



SEQUENCE LISTING

<110> SHERMAN, LINDA A.
LUSTGARTEN, JOSEPH

<120> RECOMBINANT CONSTRUCTS ENCODING T CELL RECEPTORS
SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR ANTIGENS

<130> 48340/55793

<140> 08/812,393

<141> 1997-03-05

<150> 60/012,845

<151> 1996-03-05

<160> 64

<170> PatentIn Ver. 2.1

<210> 1

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1332)

<220>

<223> Description of Artificial Sequence: Synthetic
single chain TCR derivative nucleotide sequence

<400> 1

ctc	gag	atg	cag	agg	aac	ctg	gga	gct	gtg	ctg	ggg	att	ctg	tgg	gtg	48
Leu	Glu	Met	Gln	Arg	Asn	Leu	Gly	Ala	Val	Leu	Gly	Ile	Leu	Trp	Val	
1			5						10					15		
cag	att	tgc	tgg	ctg	aaa	gaa	cag	caa	gtg	cag	cag	agt	ccc	gca	tcc	96
Gln	Ile	Cys	Trp	Leu	Lys	Glu	Gln	Gln	Val	Gln	Gln	Ser	Pro	Ala	Ser	
			20					25					30			
ttg	gtt	ctg	cag	gag	ggg	gag	aac	gca	gag	ctc	cag	tgt	agc	ttt	tcc	144
Leu	Val	Leu	Gln	Glu	Gly	Glu	Asn	Ala	Glu	Leu	Gln	Cys	Ser	Phe	Ser	
			35					40					45			
atc	ttt	aca	aac	cag	gtg	cag	tgg	ttt	tac	caa	cgt	cct	ggg	gga	aga	192
Ile	Phe	Thr	Asn	Gln	Val	Gln	Trp	Phe	Tyr	Gln	Arg	Pro	Gly	Gly	Arg	
			50				55				60					
ctc	gtc	agc	ctg	ttg	tac	aat	cct	tct	ggg	aca	aag	cag	agt	ggg	aga	240
Leu	Val	Ser	Leu	Leu	Tyr	Asn	Pro	Ser	Gly	Thr	Lys	Gln	Ser	Gly	Arg	
			65			70				75				80		
ctg	aca	tcc	aca	aca	gtc	att	aaa	gaa	cgt	cgc	agc	tct	ttg	cac	att	288
Leu	Thr	Ser	Thr	Thr	Val	Ile	Lys	Glu	Arg	Arg	Ser	Ser	Leu	His	Ile	
					85				90					95		

tcc tcc tcc cag atc aca gac tca ggc act tat ctc tgt gcc tca aat	336
Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn	
100 105 110	
tct gga gga agc aat gca aag cta acc ttc ggg aaa ggc act aaa ctc	384
Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu	
115 120 125	
tct gtt aaa tca ggt ggc gga ggg tct ggc ggg ggt gga tcc ggg ggt	432
Ser Val Lys Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly	
130 135 140	
gga ggc tca gag gct gca gtc acc caa agc cca aga aac aag gtg gca	480
Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala	
145 150 155 160	
gta aca gga gga aag gtg aca ttg agc tgt aat cag act aat aac cac	528
Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His	
165 170 175	
aac aac atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg	576
Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu	
180 185 190	
atc cat tat tca tat ggt gct ggc agc act gag aaa gga gat atc cct	624
Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro	
195 200 205	
gat gga tac aag gcc tcc aga cca agc caa gag aac ttc tcc ctc att	672
Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile	
210 215 220	
ctg gag ttg gct acc ccc tct cag aca tca gtg tac ttc tgt gcc agc	720
Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser	
225 230 235 240	
ggt gag aca ggg acc aac gaa aga tta ttt ttc ggt cat gga acc aag	768
Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys	
245 250 255	
ctg tct gtc ctg act agt aac tcc atc atg tac ttc agc cac ttc gtg	816
Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val	
260 265 270	
ccg gtc ttc ctg cca gcg aag ccc acc acg acg cca gcg ccg cga cca	864
Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro	
275 280 285	
cca aca ccg gcg ccc acc atc gcg tcg cag ccc ctg tcc ctg cgc cca	912
Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro	
290 295 300	
tct agt tct aga gat ccc aaa ctc tgc tac ctg ctg gat gga atc ctc	960
Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu	
305 310 315 320	

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ttc atc tat ggt gtc att ctc act gcc ttg ttc ctg aga gtg aag ttc 1008
Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe
325 330 335

agc agg agc gca gac gcc ccc gcg tac cag cag gcc cag aac cag ctc 1056
Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
340 345 350

tat aac gag ctc aat cta gga cga aga gag gag tac gat gtt ttg gac 1104
Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
355 360 365

aag aga cgt ggc cgg gac cct gag atg ggg gga aag ccg aga agg aag 1152
Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
370 375 380

aac cct cag gaa ggc ctg tac aat gaa ctg cag aaa gat aag atg gcg 1200
Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
385 390 395 400

gag gcc tac agt gag att ggg atg aaa ggc gag cgc cgg agg ggc aag 1248
Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
405 410 415

ggg cac gat ggc ctt tac cag ggt ctc agt aca gcc acc aag gac acc 1296
Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
420 425 430

tac gac gcc ctt cac atg cag gcc ctg ccc cct cgc taa gcg gcc gcc 1344
Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
435 440

acc gcg 1350

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<210> 2
<211> 444
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
single chain TCR protein

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<400> 2
Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val
1 5 10 15

Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser
20 25 30

Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser
35 40 45

Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg
50 55 60

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Leu	Val	Ser	Leu	Leu	Tyr	Asn	Pro	Ser	Gly	Thr	Lys	Gln	Ser	Gly	Arg		65	70	75	80
Leu	Thr	Ser	Thr	Thr	Val	Ile	Lys	Glu	Arg	Arg	Ser	Ser	Leu	His	Ile		85	90	95	
Ser	Ser	Ser	Gln	Ile	Thr	Asp	Ser	Gly	Thr	Tyr	Leu	Cys	Ala	Ser	Asn		100	105	110	
Ser	Gly	Gly	Ser	Asn	Ala	Lys	Leu	Thr	Phe	Gly	Lys	Gly	Thr	Lys	Leu		115	120	125	
Ser	Val	Lys	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly		130	135	140	
Gly	Gly	Ser	Glu	Ala	Ala	Val	Thr	Gln	Ser	Pro	Arg	Asn	Lys	Val	Ala		145	150	155	160
Val	Thr	Gly	Gly	Lys	Val	Thr	Leu	Ser	Cys	Asn	Gln	Thr	Asn	Asn	His		165	170	175	
Asn	Asn	Met	Tyr	Trp	Tyr	Arg	Gln	Asp	Thr	Gly	His	Gly	Leu	Arg	Leu		180	185	190	
Ile	His	Tyr	Ser	Tyr	Gly	Ala	Gly	Ser	Thr	Glu	Lys	Gly	Asp	Ile	Pro		195	200	205	
Asp	Gly	Tyr	Lys	Ala	Ser	Arg	Pro	Ser	Gln	Glu	Asn	Phe	Ser	Leu	Ile		210	215	220	
Leu	Glu	Leu	Ala	Thr	Pro	Ser	Gln	Thr	Ser	Val	Tyr	Phe	Cys	Ala	Ser		225	230	235	240
Gly	Glu	Thr	Gly	Thr	Asn	Glu	Arg	Leu	Phe	Phe	Gly	His	Gly	Thr	Lys		245	250	255	
Leu	Ser	Val	Leu	Thr	Ser	Asn	Ser	Ile	Met	Tyr	Phe	Ser	His	Phe	Val		260	265	270	
Pro	Val	Phe	Leu	Pro	Ala	Lys	Pro	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro		275	280	285	
Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro		290	295	300	
Ser	Ser	Ser	Arg	Asp	Pro	Lys	Leu	Cys	Tyr	Leu	Leu	Asp	Gly	Ile	Leu		305	310	315	320
Phe	Ile	Tyr	Gly	Val	Ile	Leu	Thr	Ala	Leu	Phe	Leu	Arg	Val	Lys	Phe		325	330	335	
Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu		340	345	350	
Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp		355	360	365	

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
 370 375 380

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
 385 390 395 400

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
 405 410 415

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
 420 425 430

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 435 440

<210> 3
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 3
 cccaaggcac tgatgttcac ctcc 24

<210> 4
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 4
 tgagacaaaag tccccaatct ctgacag 27

<210> 5
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 5
 ctgcagctgc tcctcaagta ctattc 26

<210> 6
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

 <400> 6
 tcccgagaa ggtccacagt tcctcttt 28

 <210> 7
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 7
 gaagcagcag agggtttgaa gccacatac 29

 <210> 8
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 8
 ggcaggtctt cagttgctta tgaaggt 27

 <210> 9
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 9
 ggttcctctt caggtccag aatatgt 27

 <210> 10
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 10
 gcgaagaact caccctggac tgttcat 27

 <210> 11
 <211> 30

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 11
 gagctccaca gacaacaaga ggacgcagca 30

<210> 12
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 12
 gagctgcgac gttccttagt gactgtg 27

<210> 13
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 13
 cctcgtcagc ctggtgtcca atccttctgg 30

<210> 14
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 14
 cagcctcatc aatctgttct acttggct 28

<210> 15
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 15
 ccaccaggga ccacagttta tcattcaa 28

<210> 16
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 16
 acctggagag aatcctaagc tcatcat 27

<210> 17
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 17
 aggtcttggtg tccctgacag tcctggtt 28

<210> 18
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 18
 caagcaaaca ctgtagtgca gagcccttcc 30

<210> 19
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 19
 caagacatcc ataactgccc tacag 25

<210> 20
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 20
 gtgtatgaaa cccaggacag ttcttac 27

<210> 21
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 21
 ccgtatttct ttcttatgtt gttttggat 29

<210> 22
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 22
 caaagctctc catcgctgac tgttcaag 28

<210> 23
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 23
 atctaattct gggaagagca aat 23

<210> 24
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 24
 ggcgctctggt accacgtggt caa 23

<210> 25
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

 <400> 25
 gtgaaagggc aaggacaaaa agc 23

 <210> 26
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 26
 gatatgcgaa cagtatctag gc 22

 <210> 27
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 27
 acataatcaa aggaaagggg gaa 23

 <210> 28
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 28
 tcctgattgg tcaggaaggg caa 23

 <210> 29
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 29
 tacctgatca aaagaatggg aga 23

 <210> 30
 <211> 23

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 30
 ataaccatga caatatgtac tgg 23

<210> 31
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 31
 ataaccacaa caacatgtac tgg 23

<210> 32
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 32
 atagccacaa ctacatgtac tgg 23

<210> 33
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 33
 agcttgcaag agttggaaaa cca 23

<210> 34
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 34
 gattatgttt agctacaata ata 23

<210> 35
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 35
acaaggtgac aggaaggga caa 23

<210> 36
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 36
acctacagaa cccaaggact cag 23

<210> 37
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 37
cagttgccct cggatcgatt ttc 23

<210> 38
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 38
gccgagatca aggctgtggg cag 23

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 39
agaaccatct gtaagagtgg aac

23

<210> 40
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 40
catcaaataa tagatatggg gca

23

<210> 41
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 41
gtagtcctga aaaagggcac act

23

<210> 42
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 42
catctgtcaa agtggcactt ca

22

<210> 43
<211> 393
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(393)

<400> 43
atg aaa tcc ttg agt gtt tcc cta gtg gtc ctg tgg ctc cag tta aac
Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn
1 5 10 15

48

tgg gtg cag agc cag cag aag gtg cag cag agc cca gaa tcc ctc agt
Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser
20 25 30

96

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gtc cca gag gga ggc atg gcc tct ctc aac tgc act tca agt gat cgc 144
Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg
      35              40              45

aat ttt cag tat ttc tgg tgg tac aga cag cat tct gga gaa ggc ccc 192
Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro
      50              55              60

aaa gca ctg atg tcc atc ttc tct gat ggt gac aag aaa gaa ggc aga 240
Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg
      65              70              75              80

ttc aca gct cac ctc aat aag gcc agc ctg cat gtt tcc ctg cac atc 288
Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile
      85              90              95

aga gac tcc cag ccc agt gac tcc gct ctc tac ttc tgt gca gtt atg 336
Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met
      100              105              110

gat tat aac cag ggg aag ctt atc ttt ggg cag ggt acc aag tta tct 384
Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser
      115              120              125

atc aag ccc 393
Ile Lys Pro
      130

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<210> 44
<211> 131
<212> PRT
<213> Homo sapiens

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<400> 44
Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn
  1              5              10              15

Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser
      20              25              30

Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg
      35              40              45

Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro
      50              55              60

Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg
      65              70              75              80

Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile
      85              90              95

Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met
      100              105              110

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Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser
 115 120 125

Ile Lys Pro
 130

<210> 45
 <211> 402
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(402)

<400> 45
 atg ggc tcc aga ctc ttc ttt gtg gtt ttg att ctc ctg tgt gca aaa 48
 Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys
 1 5 10 15

cac atg gag gct gca gtc acc caa agt cca aga agc aag gtg gca gta 96
 His Met Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val
 20 25 30

aca gga gga aag gtg aca ttg agc tgt cac cag act aat aac cat gac 144
 Thr Gly Gly Lys Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp
 35 40 45

tat atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg atc 192
 Tyr Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile
 50 55 60

cat tac tca tat gtc gct gac agc acg gag aaa gga gat atc cct gat 240
 His Tyr Ser Tyr Val Ala Asp Ser Thr Glu Lys Gly Asp Ile Pro Asp
 65 70 75 80

ggg tac aag gcc tcc aga cca agc caa gag aat ttc tct ctc att ctg 288
 Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile Leu
 85 90 95

gag ttg gct tcc ctt tct cag tca gct gta tat ttc tgt gcc agc agc 336
 Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe Cys Ala Ser Ser
 100 105 110

gat ttc gcc ggg aca ggg ggc ttc tat gaa cag tac ttc ggt ccc ggc 384
 Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly
 115 120 125

acc agg ctc acg gtt tct 402
 Thr Arg Leu Thr Val Ser
 130

<210> 46
 <211> 134

<212> PRT

<213> Homo sapiens

<400> 46

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Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys
 1           5           10           15

His Met Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val
      20           25           30

Thr Gly Gly Lys Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp
      35           40           45

Tyr Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile
      50           55           60

His Tyr Ser Tyr Val Ala Asp Ser Thr Glu Lys Gly Asp Ile Pro Asp
      65           70           75           80

Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile Leu
      85           90           95

Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe Cys Ala Ser Ser
      100          105          110

Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly
      115          120          125

Thr Arg Leu Thr Val Ser
      130

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<210> 47

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 47

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Lys Ile Phe Gly Ser Leu Ala Phe Leu
 1           5

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<210> 48

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 48

Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu
 1 5 10

<210> 49

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 peptide

<400> 49

Val Met Ala Gly Val Gly Ser Pro Tyr Val
 1 5 10

<210> 50

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 peptide

<400> 50

Val Leu Gln Gly Leu Pro Arg Glu Tyr Val
 1 5 10

<210> 51

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 peptide

<400> 51

His Leu Tyr Gln Gly Gln Trp
 1 5

<210> 52

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
 peptide

<400> 52
 Arg Leu Leu Gln Glu Thr Glu Leu Val
 1 5

<210> 53
 <211> 9
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<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 53
 Lys Ile Pro Val Ala Ile Lys Val Leu
 1 5

<210> 54
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 peptide

<400> 54
 Cys Leu Thr Ser Thr Val Gln Leu Val
 1 5

<210> 55
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 peptide

<400> 55
 Gln Leu Met Pro Tyr Gly Cys Leu Leu
 1 5

<210> 56
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<220>
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 peptide

<400> 56

Val Leu Val Lys Ser Pro Asn His Val
1 5

<210> 57

<211> 9

<212> PRT

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<223> Description of Artificial Sequence: Synthetic
peptide

<400> 57

Asp Ile Asp Glu Thr Glu Tyr His Ala
1 5

<210> 58

<211> 9

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<223> Description of Artificial Sequence: Synthetic
peptide

<400> 58

Asp Leu Leu Glu Lys Gly Glu Arg Leu
1 5

<210> 59

<211> 9

<212> PRT

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<223> Description of Artificial Sequence: Synthetic
peptide

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Glu Leu Val Ser Glu Phe Ser Arg Met
1 5

<210> 60

<211> 10

<212> PRT

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<223> Description of Artificial Sequence: Synthetic
peptide

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Glu Leu Val Ser Glu Phe Ser Arg Met Ala
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<210> 61

<211> 9

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<223> Description of Artificial Sequence: Synthetic
 peptide

<400> 61

Leu Val Ser Glu Phe Ser Arg Met Ala
 1 5

<210> 62

<211> 9

<212> PRT

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<223> Description of Artificial Sequence: Synthetic
 peptide

<400> 62

Asp Leu Val Asp Ala Glu Glu Tyr Leu
 1 5

<210> 63

<211> 9

<212> PRT

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 peptide

<400> 63

Thr Leu Ser Pro Gly Lys Asn Gly Val
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<210> 64

<211> 9

<212> PRT

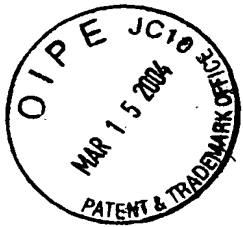
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<223> Description of Artificial Sequence: Synthetic
 peptide

<400> 64

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1 5



SEQUENCE LISTING

<110> SHERMAN, LINDA A.
LUSTGARTEN, JOSEPH

<120> RECOMBINANT CONSTRUCTS ENCODING T CELL RECEPTORS
SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR ANTIGENS

<130> 48340/55793

<140> 08/812,393

<141> 1997-03-05

<150> 60/012,845

<151> 1996-03-05

<160> 64

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<223> Description of Artificial Sequence: Synthetic
single chain TCR derivative nucleotide sequence

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1				5					10					15		
cag	att	tgc	tgg	ctg	aaa	gaa	cag	caa	gtg	cag	cag	agt	ccc	gca	tcc	96
Gln	Ile	Cys	Trp	Leu	Lys	Glu	Gln	Gln	Val	Gln	Gln	Ser	Pro	Ala	Ser	
		20						25					30			
ttg	gtt	ctg	cag	gag	ggg	gag	aac	gca	gag	ctc	cag	tgt	agc	ttt	tcc	144
Leu	Val	Leu	Gln	Glu	Gly	Glu	Asn	Ala	Glu	Leu	Gln	Cys	Ser	Phe	Ser	
		35					40					45				
atc	ttt	aca	aac	cag	gtg	cag	tgg	ttt	tac	caa	cgt	cct	ggg	gga	aga	192
Ile	Phe	Thr	Asn	Gln	Val	Gln	Trp	Phe	Tyr	Gln	Arg	Pro	Gly	Gly	Arg	
	50					55				60						
ctc	gtc	agc	ctg	ttg	tac	aat	cct	tct	ggg	aca	aag	cag	agt	ggg	aga	240
Leu	Val	Ser	Leu	Leu	Tyr	Asn	Pro	Ser	Gly	Thr	Lys	Gln	Ser	Gly	Arg	
	65				70				75					80		
ctg	aca	tcc	aca	aca	gtc	att	aaa	gaa	cgt	cgc	agc	tct	ttg	cac	att	288
Leu	Thr	Ser	Thr	Thr	Val	Ile	Lys	Glu	Arg	Arg	Ser	Ser	Leu	His	Ile	
				85					90					95		

tcc tcc tcc cag atc aca gac tca ggc act tat ctc tgt gcc tca aat	336
Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn	
100 105 110	
tct gga gga agc aat gca aag cta acc ttc ggg aaa ggc act aaa ctc	384
Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu	
115 120 125	
tct gtt aaa tca ggt ggc gga ggg tct ggc ggg ggt gga tcc ggg ggt	432
Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	
130 135 140	
gga ggc tca gag gct gca gtc acc caa agc cca aga aac aag gtg gca	480
Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala	
145 150 155 160	
gta aca gga gga aag gtg aca ttg agc tgt aat cag act aat aac cac	528
Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His	
165 170 175	
aac aac atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg	576
Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu	
180 185 190	
atc cat tat tca tat ggt gct ggc agc act gag aaa gga gat atc cct	624
Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro	
195 200 205	
gat gga tac aag gcc tcc aga cca agc caa gag aac ttc tcc ctc att	672
Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile	
210 215 220	
ctg gag ttg gct acc ccc tct cag aca tca gtg tac ttc tgt gcc agc	720
Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser	
225 230 235 240	
ggg gag aca ggg acc aac gaa aga tta ttt ttc ggt cat gga acc aag	768
Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys	
245 250 255	
ctg tct gtc ctg act agt aac tcc atc atg tac ttc agc cac ttc gtg	816
Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val	
260 265 270	
ccg gtc ttc ctg cca gcg aag ccc acc acg acg cca gcg ccg cga cca	864
Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro	
275 280 285	
cca aca ccg gcg ccc acc atc gcg tcg cag ccc ctg tcc ctg cgc cca	912
Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro	
290 295 300	
tct agt tct aga gat ccc aaa ctc tgc tac ctg ctg gat gga atc ctc	960
Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu	
305 310 315 320	

ttc atc tat ggt gtc att ctc act gcc ttg ttc ctg aga gtg aag ttc	1008
Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe	
325 330 335	
agc agg agc gca gac gcc ccc gcg tac cag cag ggc cag aac cag ctc	1056
Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu	
340 345 350	
tat aac gag ctc aat cta gga cga aga gag gag tac gat gtt ttg gac	1104
Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp	
355 360 365	
aag aga cgt ggc cgg gac cct gag atg ggg gga aag ccg aga agg aag	1152
Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys	
370 375 380	
aac cct cag gaa ggc ctg tac aat gaa ctg cag aaa gat aag atg gcg	1200
Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala	
385 390 395 400	
gag gcc tac agt gag att ggg atg aaa ggc gag cgc cgg agg ggc aag	1248
Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys	
405 410 415	
ggg cac gat ggc ctt tac cag ggt ctc agt aca gcc acc aag gac acc	1296
Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr	
420 425 430	
tac gac gcc ctt cac atg cag gcc ctg ccc cct cgc taa gcg gcc gcc	1344
Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg	
435 440	
acc gcg	1350

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 <211> 444
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 single chain TCR protein

<400> 2
Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val
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Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser
20 25 30
Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser
35 40 45
Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg
50 55 60

Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg
 65 70 75 80
 Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile
 85 90 95
 Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn
 100 105 110
 Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu
 115 120 125
 Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 130 135 140
 Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala
 145 150 155 160
 Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His
 165 170 175
 Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu
 180 185 190
 Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro
 195 200 205
 Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile
 210 215 220
 Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
 225 230 235 240
 Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys
 245 250 255
 Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val
 260 265 270
 Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro
 275 280 285
 Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
 290 295 300
 Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu
 305 310 315 320
 Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe
 325 330 335
 Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
 340 345 350
 Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
 355 360 365

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
 370 375 380
 Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
 385 390 395 400
 Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
 405 410 415
 Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
 420 425 430
 Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 435 440

<210> 3
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 3
 cccaaggcac tgatgttcat cttc

24

<210> 4
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 4
 tgagacaaaag tccccaatct ctgacag

27

<210> 5
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 5
 ctgcagctgc tcctcaagta ctattc

26

<210> 6
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

 <400> 6
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 <210> 7
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

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 <210> 8
 <211> 27
 <212> DNA
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 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 8
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 <210> 9
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 <212> DNA
 <213> Artificial Sequence

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 <400> 9
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 <210> 10
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 <212> DNA
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 <210> 11
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<212> DNA
<213> Artificial Sequence

<220>
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gagctccaca gacaacaaga ggacgcagca

30

<210> 12
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gagctgcgac gttccttagt gactgtg

27

<210> 13
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 13
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30

<210> 14
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<212> DNA
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<220>
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<400> 14
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28

<210> 15
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<400> 15
ccaccagga ccacagttta tcattcaa

28

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<400> 16
acctggagag aatcctaagc tcatcat

27

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28

<210> 18
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<400> 18
caagcaaaca ctgtagtgca gagcccttcc

30

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<220>
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<400> 19
caagacatcc ataactgccc tacag

25

<210> 20
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<400> 20
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<210> 21
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ccgtatttct ttcttatgtt gttttggat 29

<210> 22
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<400> 22
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<210> 23
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<210> 24
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ggcgtctggt accacgtggt caa 23

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 <400> 25
 gtgaaagggc aaggacaaaa agc 23

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 <210> 28
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 <210> 29
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 <212> DNA
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 <210> 30
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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<400> 35
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23

<210> 36
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 36
acctacagaa cccaaggact cag

23

<210> 37
<211> 23
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 37
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23

<210> 38
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 38
gccgagatca aggctgtggg cag

23

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 39
 agaaccatct gtaagagtgg aac 23

<210> 40
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 40
 catcaaataa tagatatggg gca 23

<210> 41
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 41
 gtagtcctga aaaagggcac act 23

<210> 42
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 42
 catctgtcaa agtggcactt ca 22

<210> 43
 <211> 393
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(393)

<400> 43
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 1 5 10 15

tgg gtg cag agc cag cag aag gtg cag cag agc cca gaa tcc ctc agt 96
 Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser
 20 25 30

gtc cca gag gga ggc atg gcc tct ctc aac tgc act tca agt gat cgc	144
Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg	
35 40 45	
aat ttt cag tat ttc tgg tgg tac aga cag cat tct gga gaa ggc ccc	192
Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro	
50 55 60	
aaa gca ctg atg tcc atc ttc tct gat ggt gac aag aaa gaa ggc aga	240
Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg	
65 70 75 80	
ttc aca gct cac ctc aat aag gcc agc ctg cat gtt tcc ctg cac atc	288
Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile	
85 90 95	
aga gac tcc cag ccc agt gac tcc gct ctc tac ttc tgt gca gtt atg	336
Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met	
100 105 110	
gat tat aac cag ggg aag ctt atc ttt ggg cag ggt acc aag tta tct	384
Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser	
115 120 125	
atc aag ccc	393
Ile Lys Pro	
130	

<210> 44
 <211> 131
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 <213> Homo sapiens

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Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser	
20 25 30	
Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg	
35 40 45	
Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro	
50 55 60	
Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg	
65 70 75 80	
Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile	
85 90 95	
Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met	
100 105 110	

Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser
 115 120 125

Ile Lys Pro
 130

<210> 45
 <211> 402
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(402)

<400> 45
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 Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys
 1 5 10 15

cac atg gag gct gca gtc acc caa agt cca aga agc aag gtg gca gta 96
 His Met Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val
 20 25 30

aca gga gga aag gtg aca ttg agc tgt cac cag act aat aac cat gac 144
 Thr Gly Gly Lys Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp
 35 40 45

tat atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg atc 192
 Tyr Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile
 50 55 60

cat tac tca tat gtc gct gac agc acg gag aaa gga gat atc cct gat 240
 His Tyr Ser Tyr Val Ala Asp Ser Thr Glu Lys Gly Asp Ile Pro Asp
 65 70 75 80

ggg tac aag gcc tcc aga cca agc caa gag aat ttc tct ctc att ctg 288
 Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile Leu
 85 90 95

gag ttg gct tcc ctt tct cag tca gct gta tat ttc tgt gcc agc agc 336
 Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe Cys Ala Ser Ser
 100 105 110

gat ttc gcc ggg aca ggg ggc ttc tat gaa cag tac ttc ggt ccc ggc 384
 Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly
 115 120 125

acc agg ctc acg gtt tct 402
 Thr Arg Leu Thr Val Ser
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<213> Homo sapiens

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His	Met	Glu	Ala	Ala	Val	Thr	Gln	Ser	Pro	Arg	Ser	Lys	Val	Ala	Val
			20					25					30		
Thr	Gly	Gly	Lys	Val	Thr	Leu	Ser	Cys	His	Gln	Thr	Asn	Asn	His	Asp
		35					40					45			
Tyr	Met	Tyr	Trp	Tyr	Arg	Gln	Asp	Thr	Gly	His	Gly	Leu	Arg	Leu	Ile
	50					55					60				
His	Tyr	Ser	Tyr	Val	Ala	Asp	Ser	Thr	Glu	Lys	Gly	Asp	Ile	Pro	Asp
65					70					75					80
Gly	Tyr	Lys	Ala	Ser	Arg	Pro	Ser	Gln	Glu	Asn	Phe	Ser	Leu	Ile	Leu
				85					90					95	
Glu	Leu	Ala	Ser	Leu	Ser	Gln	Ser	Ala	Val	Tyr	Phe	Cys	Ala	Ser	Ser
			100					105					110		
Asp	Phe	Ala	Gly	Thr	Gly	Gly	Phe	Tyr	Glu	Gln	Tyr	Phe	Gly	Pro	Gly
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Thr	Arg	Leu	Thr	Val	Ser										
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